



SEQUENCE LISTING

<110> Gurney, Mark E.
Li, Jinhe
Pauley, Adele M.
Pharmacia & Upjohn Company

RECEIVED
APR 02 2001
TECH CENTER 1600/2900

<120> Human Sel-10 Polypeptides and Polynucleotides that
Encode Them

<130> 6142

<140> 6142

<141> 1997-12-19

<160> 27

<170> PatentIn Ver. 2.0

<210> 1

<211> 3550

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2485)

<220>

<221> unsure

<222> (3372)

<400> 1

ctcattattc cctcgagttc ttctcagtcg agctgcatgt atgtatgtgt gtcccagaaa 60

Sub
D2

a

gcggtttgat actgagctgc atttgccttt actgtggagt tttgttgccg gttctgctcc 120
ctaactctcc tttctgacg tgctgagca tgtccacatt agaactctgtg acatacctac 180
ctgaaaaagg tttatattgt cagagactgc caagcagccg gacacacggg ggcacagaat 240
cactgaaggg gaaaaataca gaaaatatgg gtttctacgg cacattaana atgatttttt 300
acaaaatgaa aagaaagttg gaccatgggt ctgaggctcg ctctttttct ttgggaaaga 360
aaccatgcaa agtctcagaa tatacaagta cactgggct tgtaccatgt tcagcaacac 420
caacaacttt tggggacctc agagcagcca atggccaagg gcaacaacga cgccgaatta 480
catctgtcca gccacctaca ggctccagg aatggctaaa aatgtttcag agctggagtg 540
gaccagagaa attgcttget ttagatgaac tcattgatag ttgtgaacca acacaagtaa 600
aacatatgat gcaagtgata gaaccccagt ttcaacgaga cttcatttca ttgctcccta 660
aagagttggc actctatgtg ctttcattcc tggaaaccaa agacctgcta caagcagctc 720
agacatgtcg ctactggaga attttggtg aagacaacct tctctggaga gagaaatgca 780
aagaagaggg gattgatgaa ccattgcaca tcaagagaag aaaagtaata aaaccaggtt 840
tcatacacag tccatggaaa agtgcataca tcagacagca cagaattgat actaactgga 900
ggcgaggaga actcaaatct cctaagggtc tgaaggaca tgatgatcat gtgatcacat 960
gcttacagtt ttgtggtaac cgaatagtta gtggttctga tgacaacact ttaaaagttt 1020
ggtcagcagt cacaggcaaa tgtctgagaa cattagtggg acatacaggt ggagtatggt 1080
catcacaat gagagacaac atcatcatta gtggatctac agatcggaca ctcaaagtgt 1140
ggaatgcaga gactggagaa tgtatacaca ccttatatgg gcatacttcc actgtgcggt 1200
gtatgcatct tcatgaaaaa agagttgtta gcggttctcg agatgccact cttagggttt 1260
gggatattga gacaggccag tgtttacatg ttttgatggg tcatgttgca gcagtccgct 1320
gtgttcaata tgatggcagg agggttgtta gtggagcata tgattttatg gtaaagggtg 1380
gggatccaga gactgaaacc tgtctacaca cgttgcaggg gcatactaat agagtctatt 1440
cattacagtt tgatggatc catgtgggtga gtggatctct tgatacatca atccgtgttt 1500
gggatgtgga gacagggaat tgcattcaca cgttaacagg gcaccagtcg ttaacaagtg 1560
gaatggaact caagacaat attcttgtct ctgggaatgc agattctaca gttaaaatct 1620
gggatatcaa aacaggacag tgtttacaaa cattgcaagg tccaacaag catcagagtg 1680
ctgtgacctg ttacagttc aacaagaact ttgtaattac cagctcagat gatggaactg 1740
taaaactatg ggacttgaaa acgggtgaat ttattcgaaa ctagtcaca ttggagagtg 1800
gggggagtgg gggagttgtg tggcggatca gagcctcaaa cacaaagctg gtgtgtgcag 1860
ttgggagtgc gaatgggact gaagaaacca agctgctggt gctggacttt gatgtggaca 1920

Sub
D2

tgaagtgaag agcagaaaag atgaatttgt ccaattgtgt agacgatata ctccctgccc 1980
 ttccccctgc aaaaagaaaa aaagaaaaga aaaagaaaa aatcccttgt tctcagtgg 2040
 gcaggatggt ggcttggggc aacagattga aaagacctac agactaagaa ggaaaagaag 2100
 aagagatgac aaaccataac tgacaagaga ggcgtctgct gtctcatcac ataaaaggct 2160
 tcacttttga ctgagggcag ctttgcaaaa tgagactttc taaatcaaac caggtgcaat 2220
 tatttcttta ttttcttctc cagtgggtcat tggggcagtg ttaatgctga aacatcatta 2280
 cagattctgc tagcctgttc ttttaccact gacagctaga cacctagaaa ggaactgcaa 2340
 taatatcaaa acaagtactg gttgactttc taattagaga gcatctgcaa caaaaagtca 2400
 tttttctgga gtggaaaagc ttaaaaaaat tactgtgaat tgtttttgta cagttatcat 2460
 gaaaagcttt tttttttatt ttttngccaa ccattgccaa tgtcaatcaa tcacagtatt 2520
 agcctctgtt aatctattta ctggtgcttc catatacatt cttcaatgca tatggtgctc 2580
 aaaggtggca agttgtcctg ggttctgtga gtcctgagat ggatttaatt cttgatgctg 2640
 gtgctagaag taggtcttca aatatgggat tgttgcctca accctgtact gtactcccag 2700
 tggccaaact tatttatgct gctaaatgaa agaaagaaaa aagcaaatta ttttttttat 2760
 ttttttctg ctgtgacgtt ttagtcccag actgaattcc aaatttgctc tagtttggtt 2820
 atggaaaaaa gactttttgc cactgaaact tgagccatct gtgcctctaa gaggctgaga 2880
 atggaagagt ttcagataat aaagagtgaa gtttgctgctc aagtaaagaa ttgagagtg 2940
 gtgcaaagct tattttcttt tatctgggca aaaattaaaa cacattcctt ggaacagagc 3000
 tattacttgc ctgttctgtg gagaaacttt tctttttgag ggctgtgggtg aatggatgaa 3060
 cgtacatcgt aaaactgaca aaatatttta aaaatatata aaacacaaaa ttaaaataaa 3120
 gttgctggtc agtcttagtg ttttacagta tttgggaaaa caactgttac agttttattg 3180
 ctctgagtaa ctgacaaagc agaaactatt cagtttttgt agtaaaggcg tcacatgcaa 3240
 acaaacaaaa tgaatgaaac agtcaaagtg tttgcctcat tctccaagag ccacaactca 3300
 agctgaactg tgaaagtggg ttaacactgt atcctaggcg atcttttttc ctcttctgt 3360
 ttattttttt gnttgtttta tttatagtct gatttaaaac aatcagattc aagttgggta 3420
 attttagtta tgtaacaacc tgacatgatg gaggaaaaca acctttaaag ggattgtgct 3480
 tatggtttga ttcacttaga aattttattt tcttataact taagtgcaat aaaatgtggt 3540
 ttttcatggt 3550

Sub
D2

<210> 2

<211> 3571

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2506)

<220>

<221> unsure

<222> (3393)

<400> 2

ctcagcaggt caggacattt ggtaggggaa ggttgaaaga caaaagcagc aggccttggg 60
ttctcagcct tttaaaaact attattaaat atatattttt aaaatttagt ggtagagct 120
tttagtaatg tgctgtatt acatgtagag agtattcgtc aaccaagagg agtttataaa 180
tgtcaaaacc gggaaaacct actctaaacc atggcttggg tctgttgat cttaaagtg 240
caaaagagcc tctaccacat caaacctga tgaagatatt tagcattagc atcattgcc 300
aaggcctccc tttttgtcga agacggatga aaagaaagt ggaccatggg tctgaggtcc 360
gctctttttc tttgggaaag aaaccatgca aagtctcaga atatacaagt accactgggc 420
ttgtaccatg ttcagcaaca ccaacaactt ttggggacct cagagcagcc aatggccaag 480
ggcaacaacg acgccgaatt acatctgtcc agccacctac aggcctccag gaatggctaa 540
aatgtttca gagctggagt ggaccagaga aattgcttgc ttagatgaa ctattgata 600
gttgatgaacc aacacaagta aaacatatga tgcaagtgat agaaccctcag tttcaacgag 660
acttcatttc attgctccct aaagagttgg cactctatgt gctttcattc ctggaacca 720
aagacctgct acaagcagct cagacatgct gctactggag aattttggct gaagacaacc 780
ttctctggag agagaaatgc aaagaagagg ggattgatga accattgcac atcaagagaa 840
gaaaagtaat aaaaccaggt ttcatacaca gtccatggaa aagtgcatac atcagacagc 900
acagaattga tactaactgg aggcgaggag aactcaaact tcctaagggt ctgaaaggac 960
atgatgatca tgtgatcaca tgcttacagt tttgtggtaa ccgaatagtt agtggttctg 1020
atgacaacac tttaaaagtt tggtcagcag tcacaggcaa atgtctgaga acattagtgg 1080
gacatacagg tggagtatgg tcatcaciaa tgagagacia catcatcatt agtggatcta 1140
cagatcggac actcaaagtg tggaatgcag agactggaga atgtatacac accttatatg 1200
ggcatacttc cactgtgcgt tgtatgcac ttcatgaaaa aagagttggt agcggttctc 1260

Self
D2

gagatgccac tcttaggggtt tgggatattg agacaggcca gtgtttacat gttttgatgg 1320
gtcatgttgc agcagtcocgc tgtgttcaat atgatggcag gagggttggt agtggagcat 1380
atgattttat ggtaaagggtg tgggatccag agactgaaac ctgtctacac acgttgcagg 1440
ggcatactaa tagagtctat tcattacagt ttgatgggat ccatgtgggtg agtggatctc 1500
ttgatacatc aatccgtggt tgggatgtgg agacagggaa ttgcattcac acgttaacag 1560
ggcaccagtc gttaacaagt ggaatggaac tcaaagacia tattcttgtc tctgggaatg 1620
cagattctac agttaaatac tgggatatca aacaggaca gtgtttacia acattgcaag 1680
gtcccaacia gcatcagagt gctgtgacct gtttacagtt caacaagaac tttgtaatta 1740
ccagctcaga tgatggaact gtaaaactat gggacttgaa aacgggtgaa tttattcgaa 1800
acctagtcac attggagagt ggggggagtg ggggagttgt gtggcggatc agagcctcaa 1860
acaciaagct ggtgtgtgca gttgggagtc ggaatgggac tgaagaaacc aagctgctgg 1920
tgctggactt tgatgtggac atgaagtga gagcagaaaa gatgaatttg tccaattgtg 1980
tagacgatat actccctgcc cttccccctg caaaaagaaa aaaagaaaag aaaaagaaaa 2040
aatcccttg ttctcagtg tgcaggatgt tggcttgggg caacagattg aaaagaccta 2100
cagactaaga aggaaaagaa gaagagatga caaacataa ctgacaagag aggcgtctgc 2160
tgtctcatca cataaaaggc ttcacttttg actgagggca gctttgcaaa atgagacttt 2220
ctaaatcaaa ccaggtgcaa ttatttcttt attttcttct ccagtggtca ttggggcagt 2280
gttaatgctg aaacatcatt acagattctg ctagcctggt cttttaccac tgacagctag 2340
acacctagaa aggaactgca ataatatcaa aacaagtact ggttgacttt ctaattagag 2400
agcatctgca acaaaaagtc attttctg agtggaagag cttaaaaaaa ttactgtgaa 2460
ttgtttttgt acagttatca tgaaaagctt ttttttttat tttttngcca accattgcca 2520
atgtcaatca atcacagtat tagcctctgt taatctattt actggtgctt ccatatacat 2580
tcttcaatgc atatgttgct caaagggtggc aagttgtcct gggttctgtg agtcctgaga 2640
tggatttaat tcttgatgct ggtgctagaa gtaggtcttc aaatatggga ttggtgtccc 2700
aaccctgtac tgtactecca gtggccaaac ttatttatgc tgctaaatga aagaaagaaa 2760
aaagcaaatt atttttttta tttttttct gctgtgacgt ttagtccca gactgaattc 2820
caaatttgct ctagtgtgt tatggaaaa agacttttg cactgaaac ttgagccatc 2880
tgtgcctcta agaggctgag aatggaagag tttcagataa taaagagtga agtttgctg 2940
caagtaaaga attgagagt tgtgcaaagc ttatttctt ttatctgggc aaaaattaa 3000
acacattcct tggaacagag ctattacttg cctgttctgt ggagaaactt ttctttttga 3060
gggctgtggt gaatggatga acgtacatcg taaaactgac aaaatattt aaaaatatat 3120

aaaacacaaa attaaaataa agttgctggt cagtcttagt gttttacagt atttgggaaa 3180
 acaactgtta cagttttatt gctctgagta actgacaaaag cagaaactat tcagtttttg 3240
 tagtaaaggc gtcacatgca aacaaacaaa atgaatgaaa cagtcaaag gtttgcctca 3300
 ttctccaaga gccacaactc aagctgaact gtgaaagtgg tttaacactg tctcctagc 3360
 gatctttttt cctccttctg tttatTTTTT tgnttgTTTT atttatagtc tgatttaaaa 3420
 caatcagatt caagttgggt aatttttagtt atgtaacaac ctgacatgat ggaggaaaac 3480
 aacctttaa gggattgtgt ctatggtttg attcacttag aaattttatt ttcttataac 3540
 ttaagtgcaa taaaatgtgt tttttcatgt t 3571

<210> 3

<211> 627

<212> PRT

<213> Homo sapiens

<400> 3

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr
 1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr
 20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys
 35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
 50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
 65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

100

105

110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115

120

125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

130

135

140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145

150

155

160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

165

170

175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

180

185

190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

195

200

205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala

210

215

220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

225

230

235

240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

245

250

255

*Sub
D2*

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580

585

590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser

595

600

605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val

610

615

620

Asp Met Lys

625

<210> 4

<211> 592

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys Gly Leu Tyr

1

5

10

15

Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr Glu Ser Leu

20

25

30

Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr Leu Lys Met

35

40

45

Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg

50

55

60

Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser

*Sub
D2*

65

70

75

80

Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp

85

90

95

Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser

100

105

110

Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser

115

120

125

Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser

130

135

140

Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln

145

150

155

160

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr

165

170

175

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr

180

185

190

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu

195

200

205

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg

210

215

220

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr

225

230

235

240

*Sol
D2*

Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys

245 250 255

Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu

260 265 270

Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu

275 280 285

Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly

290 295 300

His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile

305 310 315 320

Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly

325 330 335

Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met

340 345 350

His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu

355 360 365

Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly

370 375 380

His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val

385 390 395 400

Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu
405 410 415

Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu
420 425 430

Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile
435 440 445

Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly
450 455 460

His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val
465 470 475 480

Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly
485 490 495

Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val
500 505 510

Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp
515 520 525

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn
530 535 540

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile
545 550 555 560

Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly

*Sub
D2*

565

570

575

Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

580

585

590

<210> 5

<211> 553

<212> PRT

<213> Homo sapiens

<400> 5

Met Gly Phe Tyr Gly Thr Leu Lys Met Ile Phe Tyr Lys Met Lys Arg

1

5

10

15

Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu Gly Lys Lys

20

25

30

Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys

35

40

45

Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln

50

55

60

Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro Thr Gly Leu

65

70

75

80

Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu

Sub
D2

85

90

95

Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr Gln Val Lys

100

105

110

His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser

115

120

125

Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro

130

135

140

Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu

145

150

155

160

Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile

165

170

175

Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys Pro Gly Phe

180

185

190

Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His Arg Ile Asp

195

200

205

Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val Leu Lys Gly

210

215

220

His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile

225

230

235

240

Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser Ala Val Thr

245

250

255

Sub
D2

Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly Val Trp Ser
260 265 270

Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr
275 280 285

Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His Thr Leu Tyr
290 295 300

Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu Lys Arg Val
305 310 315 320

Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr
325 330 335

Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala Val Arg Cys
340 345 350

Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met
355 360 365

Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr Leu Gln
370 375 380

Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly Ile His Val
385 390 395 400

Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Val Glu Thr
405 410 415

Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu Thr Ser Gly
420 425 430

Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr
435 440 445

Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln
450 455 460

Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln Phe Asn Lys
465 470 475 480

Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp
485 490 495

Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu Glu Ser Gly
500 505 510

Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu
515 520 525

Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu
530 535 540

Val Leu Asp Phe Asp Val Asp Met Lys
545 550

<210> 6

<211> 545

<212> PRT

<213> Homo sapiens

<400> 6

Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val

1 5 10 15

Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr

20 25 30

Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly

35 40 45

Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr

50 55 60

Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln

65 70 75 80

Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp

85 90 95

Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro

100 105 110

Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu

115 120 125

Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln

130 135 140

Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg

Sub
D2

145		150		155		160
Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg						
	165		170		175	
Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala						
	180		185		190	
Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu						
	195		200		205	
Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys						
	210		215		220	
Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr						
	225		230		235	
Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val						
	245		250		255	
Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile						
	260		265		270	
Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr						
	275		280		285	
Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys						
	290		295		300	
Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr						
	305		310		315	
						320

Sol
D2

Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met

325 330 335

Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val

340 345 350

Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr

355 360 365

Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser

370 375 380

Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser

385 390 395 400

Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr

405 410 415

Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu

420 425 430

Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr

435 440 445

Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala

450 455 460

Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp

465 470 475 480

Sub
D2

Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg
485 490 495

Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg
500 505 510

Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn
515 520 525

Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met
530 535 540

Lys
545

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu
1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu
20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala
35 40 45

Sub
D2

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro
 50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro
 65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr
 85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp
 100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe
 115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp
 130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu
 145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys
 165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His
 180 185 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val
 195 200 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly

Sub
D2

Sub
D2

210		215		220
Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser				
225		230		235 240
Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly				
	245		250	255
Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr				
	260		265	270
Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His				
	275		280	285
Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu				
	290		295	300
Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp				
305		310		315 320
Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala				
	325		330	335
Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr				
	340		345	350
Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His				
	355		360	365
Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly				
	370		375	380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu
405 410 415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala
420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln
435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln
450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys
465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu
485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr
515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
530 535 540

Sub
D2

<210> 8

<211> 589

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Lys Pro Gly Lys Pro Thr Leu Asn His Gly Leu Val Pro Val

1 5 10 15

Asp Leu Lys Ser Ala Lys Glu Pro Leu Pro His Gln Thr Val Met Lys

20 25 30

Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys Arg Arg

35 40 45

Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser

50 55 60

Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly

65 70 75 80

Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala

85 90 95

Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro

100 105 110

Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly

115 120 125

Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro
 130 135 140

Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg
 145 150 155 160

Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser
 165 170 175

Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr
 180 185 190

Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys
 195 200 205

Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile
 210 215 220

Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln
 225 230 235 240

His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys
 245 250 255

Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys
 260 265 270

Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp
 275 280 285

Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly

Sub
D2

Sub
D2

290						295										300
Gly	Val	Trp	Ser	Ser	Gln	Met	Arg	Asp	Asn	Ile	Ile	Ile	Ser	Gly	Ser	
305					310					315					320	
Thr	Asp	Arg	Thr	Leu	Lys	Val	Trp	Asn	Ala	Glu	Thr	Gly	Glu	Cys	Ile	
				325					330					335		
His	Thr	Leu	Tyr	Gly	His	Thr	Ser	Thr	Val	Arg	Cys	Met	His	Leu	His	
			340					345					350			
Glu	Lys	Arg	Val	Val	Ser	Gly	Ser	Arg	Asp	Ala	Thr	Leu	Arg	Val	Trp	
		355						360				365				
Asp	Ile	Glu	Thr	Gly	Gln	Cys	Leu	His	Val	Leu	Met	Gly	His	Val	Ala	
		370				375						380				
Ala	Val	Arg	Cys	Val	Gln	Tyr	Asp	Gly	Arg	Arg	Val	Val	Ser	Gly	Ala	
385					390					395					400	
Tyr	Asp	Phe	Met	Val	Lys	Val	Trp	Asp	Pro	Glu	Thr	Glu	Thr	Cys	Leu	
				405					410					415		
His	Thr	Leu	Gln	Gly	His	Thr	Asn	Arg	Val	Tyr	Ser	Leu	Gln	Phe	Asp	
			420					425					430			
Gly	Ile	His	Val	Val	Ser	Gly	Ser	Leu	Asp	Thr	Ser	Ile	Arg	Val	Trp	
		435						440				445				
Asp	Val	Glu	Thr	Gly	Asn	Cys	Ile	His	Thr	Leu	Thr	Gly	His	Gln	Ser	
		450				455						460				

Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn
465 470 475 480

Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu
485 490 495

Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu
500 505 510

Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val
515 520 525

Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr
530 535 540

Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser
545 550 555 560

Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu
565 570 575

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
580 585

<210> 9

<211> 559

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys

1 5 10 15

Arg Arg Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser

20 25 30

Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr

35 40 45

Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu

50 55 60

Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val

65 70 75 80

Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp

85 90 95

Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys

100 105 110

Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe

115 120 125

Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val

130 135 140

Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys

145 150 155 160

Ser
D2

Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys
165 170 175

Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys
180 185 190

Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile
195 200 205

Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser
210 215 220

Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln
225 230 235 240

Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys
245 250 255

Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His
260 265 270

Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser
275 280 285

Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu
290 295 300

Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His
305 310 315 320

Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg

Sark
D2

325

330

335

Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His

340

345

350

Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser

355

360

365

Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr

370

375

380

Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln

385

390

395

400

Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg

405

410

415

Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His

420

425

430

Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser

435

440

445

Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln

450

455

460

Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr

465

470

475

480

Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly

485

490

495

Sub
D2

Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu

500 505 510

Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg

515 520 525

Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr

530 535 540

Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

545 550 555

<210> 10

<211> 540

<212> PRT

<213> Homo sapiens

<400> 10

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala

35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro

50 55 60

Sub D2

Sel
D2

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro
65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr
85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp
100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe
115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp
130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu
145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys
165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His
180 185 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val
195 200 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser
225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
275 280 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu
290 295 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp
305 310 315 320

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr
340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp

Sent
DZ

385

390

395

400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu

405

410

415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala

420

425

430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln

435

440

445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln

450

455

460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys

465

470

475

480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu

485

490

495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn

500

505

510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr

515

520

525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

530

535

540

<210> 11

Sol
D2

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 11

cgggatccac catggatgat ggatcgatga cacc

34

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 12

ggaattcctt aagggtatac agcatcaaag tcg

33

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 13

tcacttcatg tccacatcaa agtcc

25

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 14

ggtaattaca agttcttggt gaactg

26

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 15

ccctgcaacg tgtgtagaca gg

22

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 16

ccagtctctg cattccacac ttg

24

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 17

ctcagacagg tcaggacatt tgg

23

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 18

ggaattccat gaaaagattg gaccatggtt ctg

33

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 19

ggaattcctc acttcatgtc acatcaaagt ccag

34

<210> 20

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged

homo sapiens

<400> 20

atggagcaaa agctcatttc tgaagaggac ttgaatgaaa tggagcaaaa gctcatttct 60
gaagaggact tgaatgaaat ggagcaaaag ctcatctctg aagaggactt gaatgaaatg 120
gagcaaaaagc tcatttctga agaggacttg aatgaaatgg agcaaaaagct catttctgaa 180
gaggacttga atgaaatgga gagcttgggc gacctcacca tggagcaaaa gctcatttct 240
gaagaggact tgaattccat gaaaagaaag ttggaccatg gttctgaggt ccgctctttt 300
tctttgggaa agaaaccatg caaagtctca gaatatacaa gtaccactgg gcttgtacca 360
tgttcagcaa caccaacaac ttttggggac ctgagagcag ccaatggcca agggcaacaa 420

cgagcgcgaa ttacatctgt ccagccacct acaggcctcc aggaatggct aaaaatgttt 480
 cagagctgga gtggaccaga gaaattgctt gctttagatg aactcattga tagttgtgaa 540
 ccaacacaag taaaacatat gatgcaagtg atagaacccc agtttcaacg agacttcatt 600
 tcattgctcc ctaaagagtt ggcactctat gtgctttcat tcttgaacc caaagacctg 660
 ctacaagcag ctcagacatg tcgctactgg agaattttgg ctgaagacaa ccttctctgg 720
 agagagaaat gcaaagaaga ggggattgat gaaccattgc acatcaagag aagaaaagta 780
 ataaaaccag gtttcataca cagtccatgg aaaagtgcac acatcagaca gcacagaatt 840
 gatactaact ggagggcagg agaactcaaa tctcctaagg tgctgaaagg acatgatgat 900
 catgtgatca catgcttaca gttttgtggt aaccgaatag ttagtgggtc tgatgacaac 960
 actttaaag tttggtcagc agtcacaggc aatgtctga gaacattagt gggacataca 1020
 ggtggagtat ggtcatcaca aatgaggac aacatcatca ttagtggatc tacagatcgg 1080
 aactcaaag tgtggaatgc agagactgga gaatgtatac acaccttata tgggcatact 1140
 tccactgtgc gttgtatgca tcttcatgaa aaaagagttg ttagcgggtc tcgagatgcc 1200
 actcttaggg tttgggatat tgagacaggc cagtgtttac atgttttgat gggatcatgtt 1260
 gcagcagtc gctgtgttca atatgatggc aggagggttg ttagtggagc atatgatttt 1320
 atggtaaagg tgtgggatcc agagactgaa acctgtctac acacgttgca ggggcatact 1380
 aatagagtct attcattaca gtttgatggt atccatgtgg tgagtggatc tcttgataca 1440
 tccatccgtg tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag 1500
 tcgttaacaa gtggaatgga actcaaagac aatattcttg tctctgggaa tgcagattct 1560
 acagttaaaa tctgggatat caaaacagga cagtgtttac aaacattgca aggtcccaac 1620
 aagcatcaga gtgctgtgac ctgtttacag ttcaacaaga actttgtaat taccagctca 1680
 gatgatggaa ctgtaaaact atgggacttg aaaacgggtg aatttattcg aaacctagtc 1740
 acattggaga gtggggggag tgggggagtt gtgtggcgga tcagagcctc aaacacaaag 1800
 ctggtgtgtg cagttgggag tcggaatggg actgaagaaa ccaagctgct ggtgctggac 1860
 tttgatgtgg acatgaagtg a 1881

<210> 21

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged

homo sapien

<400> 21

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln

1 5 10 15

Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile

20 25 30

Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu

35 40 45

Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

50 55 60

Glu Met Glu Ser Leu Gly Asp Leu Thr Met Glu Gln Lys Leu Ile Ser

65 70 75 80

Glu Glu Asp Leu Asn Ser Met Lys Arg Lys Leu Asp His Gly Ser Glu

85 90 95

Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr

100 105 110

Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe

115 120 125

Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile

130 135 140

Set
D2

Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe
145 150 155 160

Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile
165 170 175

Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu
180 185 190

Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala
195 200 205

Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala
210 215 220

Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp
225 230 235 240

Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys
245 250 255

Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser
260 265 270

Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu
275 280 285

Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr
290 295 300

Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn
305 310 315 320

Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu
325 330 335

Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile
340 345 350

Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu
355 360 365

Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg
370 375 380

Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala
385 390 395 400

Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu
405 410 415

Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg
420 425 430

Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu
435 440 445

Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr
450 455 460

Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr

Self
D2

465

470

475

480

Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu

485

490

495

Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile

500

505

510

Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys

515

520

525

Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser

530

535

540

Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser

545

550

555

560

Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile

565

570

575

Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp

580

585

590

Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg

595

600

605

Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp

610

615

620

Met Lys

625

Sub
D2

<210> 22

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 22

gggtaccctt cattattccc tcgagttctt c

31

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 23

ggaattcctt catgtccaca tcaaagtcc

29

<210> 24

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

<400> 24

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60
ttgccgggtc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240
ttaaaaatga ttttttacia aatgaaaaga aagttggacc atggttctga ggtccgctct 300
ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480
tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600
atttcattgc tcctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660
ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780
gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900
gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960
aacactttaa aagtttggtc agcagtcaca ggcaaagtgc tgagaacatt agtgggacat 1020
acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080
cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140
acttccactg tgcgttgat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200
gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320
tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380
actaatagag tctattcatt acagtttgat ggtatccatg tggtgagtgg atctcttgat 1440
acatcaatcc gtgtttggga tgtggagaca gggaaattgca ttcacacgtt aacagggcac 1500
cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560

tctacagtta aaatctggga tatcaaaaca ggacagtgtt taaaacatt gcaaggtccc 1620
 aacaagcatc agagtgtgtg gacctgttta cagttcaaca agaactttgt aattaccagc 1680
 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740
 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800
 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
 tctagagggc cttcgaagg taagcctatc cctaaccctc tctcgggtct cgattctacg 1980
 cgtaccggtc atcatcacca tcaccattga 2010

<210> 25

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

<400> 25

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser
85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

Sel
DZ

225

230

235

240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

245

250

255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260

265

270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

275

280

285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

290

295

300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305

310

315

320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

325

330

335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340

345

350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355

360

365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

370

375

380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385

390

395

400

Sub
D2

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
545 550 555 560

Seq
D2

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val
580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu
625 630 635 640

Ser Arg Gly Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
645 650 655

Leu Asp Ser Thr Arg Thr Gly His His His His His His
660 665

<210> 26

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged

homo sapiens

<400> 26

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60
ttgceggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240
ttaaaaaatga ttttttaciaa aatgaaaaga aagttggacc atggttctga ggtccgctct 300
ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480
tttcagagct ggagtgacc agagaaattg cttgctttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600
atttcattgc tcctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660
ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaacctat tgcacatcaa gagaagaaaa 780
gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900
gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960
aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020
acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080
cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140
acttccactg tgcgttgat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200
gccactcta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320
tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacggt gcaggggcat 1380
actaatagag tctattcatt acagtttgat ggtatccatg tggtgagtgg atctcttgat 1440
acatcaatcc gtgtttggga tgtggagaca ggaattgca ttcacacggt aacagggcac 1500
cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560
tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaacatt gcaaggtccc 1620
aacaagcatc agagtgtgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680
tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740
gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800

Sub
D2

aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctgggtgctg 1860
gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
tctagagggc ctttcgaaca aaaactcatc tcagaagagg atctgaatat gcataccggt 1980
catcatcacc atcaccattg a 2001

<210> 27

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged
homo sapiens

<400> 27

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85

90

95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

100

105

110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115

120

125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

130

135

140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145

150

155

160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

165

170

175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

180

185

190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

195

200

205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala

210

215

220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

225

230

235

240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

245

250

255

Sub D2

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val
450 455 460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp
465 470 475 480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr
485 490 495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn
500 505 510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile
515 520 525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln
530 535 540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser
545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe
565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580

585

590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser

595

600

605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val

610

615

620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu

625

630

635

640

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

645

650

655

Met His Thr Gly His His His His His His

660

665

RECEIVED

APR 02 2001

TECH CENTER 1600/2900

1

3